

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: June 23, 2003, 08:31:36 ; Search time 41.0409 Seconds
(without alignments)
431.003 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964
Sequence: 1 MLOMAGQCSQNEYPDSLHA.....CKSLPALSAITEIKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	964	100.0	184	2 S43486	B-cell maturation
2	88.5	9.2	217	2 C97344	amino acid ABC tra
3	86.5	9.0	858	2 T08881	prominin - mouse
4	83.5	8.7	1998	2 T13009	hypothetical prote
5	82	8.5	1009	2 A57434	protein-tyrosine k
6	81.5	8.5	2233	2 T28669	surface protein 51
7	81	8.4	773	2 D89010	protein R08f1.7 l
8	79.5	8.2	1009	2 S60248	protein-tyrosine k
9	79.5	8.2	1299	2 T43251	furin (EC 3.4.21.7
10	78.5	8.1	343	2 D64469	potassium channel
11	78	8.1	841	2 UC5894	killer cell inhibi
12	77.5	8.0	738	2 D86345	hypothetical prote
13	77.5	8.0	968	2 T01733	hypothetical prote
14	77.5	8.0	522	2 T45824	hypothetical prote
15	77	8.0	539	2 F72288	hypothetical prote
16	76.5	7.9	357	2 T2152	hypothetical prote
17	76.5	7.9	1404	2 T19277	hypothetical prote
18	76	7.9	744	2 A4353	asectes sialoglyco
19	76	7.9	748	2 T47250	complex I intermed
20	75.5	7.8	638	2 T41478	probable transcrip
21	75	7.8	450	2 B97297	hydrogenase chain
22	75	7.8	857	1 A41369	S-receptor kinase
23	74.5	7.7	384	2 S45592	ERD1 protein - yea
24	74.5	7.7	1101	2 T16840	hypothetical prote
25	74	7.7	377	2 UC7535	chitinase (EC 3.2.
26	73.5	7.6	307	2 B95099	membrane protein l
27	73.5	7.6	307	2 A97967	conserved hypothet
28	73	7.6	304	2 A89882	hypothetical prote
29	73	7.6	679	2 B96599	protein P20N2.12 l

30	73	7.6	733	1 A46373	probable serine/tn
31	72.5	7.5	243	2 T31144	hypothetical prote
32	72.5	7.5	408	2 B84518	hypothetical prote
33	72	7.5	416	2 S75097	hypothetical prote
34	72	7.5	855	2 T10665	hypothetical prote
35	71.5	7.4	105	2 T10350	hypothetical prote
36	71.5	7.4	627	2 B71709	conserved hypothet
37	71	7.4	227	2 F72334	hypothetical prote
38	71	7.4	414	2 G71331	probable cell divi
39	71	7.4	473	2 A91207	ABC transporters l
40	71	7.4	480	2 G88690	protein F41H0.1 l
41	71	7.4	500	2 T10543	hypothetical prote
42	71	7.4	600	2 T02768	spike glycoprotein
43	70.5	7.3	188	2 H82933	hypothetical prote
44	70.5	7.3	412	2 T24023	hypothetical prote
45	70.5	7.3	424	2 T14525	S1-locus-specific g

ALIGNMENTS

RESULT 1

S43486

B-cell maturation factor - human

N:Alternate names: BCM protein; BCM protein; BEL protein

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 21-Jul-2000

C:Accession: S43486; S31208; S36661

R:Liabli, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.

Nucleic Acids Res. 22, 1147-1154, 1994

A>Title: The BCM gene, preferentially expressed during B lymphoid maturation, is bidire

A:Reference number: S43486; MUID:9421835; PMID:8165126

A:Accession: S43486

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-184 <LAA>

A:Cross-references: EMBL:Z29574; NID:G471244; PIDN:CA82690.1; PID:G471245

R:Liabli, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis,

EMBO J. 11, 3897-3904, 1992

A>Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;1

A:Reference number: S31208; MUID:93010984; PMID:1396583

A:Accession: S31208

A:Molecule type: mRNA

A:Residues: 1-184 <LAA>

A:Cross-references: EMBL:Z14954; NID:G29407; PIDN:CA78679.1; PID:G29408

A:Accession: S36661

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 4-184 <LAA>

A:Cross-references: EMBL:Z14955

C:Genetics:

A:Gene: GDB:BCMA

A:Cross-references: GDB:135977; OMIM:109545

A:Map position: 16p13.1-16p13.1

A:introns: 44/1; 93/1

C:Superfamily: human B-cell maturation factor

Query Match

Best Local Similarity 100.0%; Pred. No. 5.6e-81;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPTLCORYCNASVTSVKGNNIILMTCL	60
DB	1	MLOMAGQCSQNEYPDSLHACIPCOLRCSSNTPPTLCORYCNASVTSVKGNNIILMTCL	60
QY	61	GLSLIISLAVFLVFLFKRISSEPLKDFKNTGSLGGLGMANIDERSRTGDEIILPGLA	120
DB	61	GLSLIISLAVFLVFLFKRISSEPLKDFKNTGSLGGLGMANIDERSRTGDEIILPGLA	120
QY	121	YVBERCTCEDICIKSKPKVDSDHCPPLPAMEGATITLVTTKNDYCKSLPALSAITEIKS	180
DB	121	YVBERCTCEDICIKSKPKVDSDHCPPLPAMEGATITLVTTKNDYCKSLPALSAITEIKS	180

QY 181 ISAR 184
Db 181 ISAR 184

RESULT 2

amino acid ABC transporter, permease component CAC3619 (imported) - Clostridium acetobutylicum C97344
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C/Accession: C97344
R/Molling, J.; Breton, G.; Omeilenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C
A/Reference number: A96900; PMID:21359325; PMID:21359325
A/Accession: C97344
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-217 <R>
A/Experimental source: GB:AE001437; PIDN:AAK81542.1; PID:GL5026719; GSPDB:GN00168
C/Genetics:
A/Genes: CAC3619
C/Superfamily: histidine permease protein M

Query Match 9.2%; Score 88.5; DB 2; Length 217;
Best Local Similarity 24.8%; Pred. No. 0.98; Indels 65; Gaps 10;
Matches 55; Conservative 25; Mismatches 77;

QY 16 SLHACIPCOLRCSNTPTTCORCNASV-----TNSVKGNTAI---LMTCLG 62
Db 4 SLSNKVIPVLDGTRITLLTSSIIICIGITIMFKTSSVKVNLGKFPYTLRGT 63
QY 63 SLIISLAIVFV--LMFLRKISSEPLADEF---KATGS-----GLGMANIDLEKSR 108
Db 64 PLILQIVYVYGGPFLSDKLTMTMPKAAIIGLSNGAVYIAIRIGIILADINGOFEASK 123
QY 109 -----TGDEIILRGLEYTVEEC-----TCEDCI-KSKPKYDSDH 142
Db 124 ALGLTGTGQWKRIILPOLNVVIPCGNEFIAMIKDTSLVSVTMEELKAKOLLVSSGS 183
QY 143 CPELPAMEGA--TIVTTKTNDYCKSLPAALSAIEIKSIS 182
Db 184 DATVPLFAGIFVILITITFTGFSK-----IEKKLS 215

RESULT 3

QY 181
Db 181
C/Species: Mus musculus (house mouse)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: T08881
R/Welgmann, A.; Corbell, D.; Hellwig, A.; Hutterer, W.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A/Title: Prominin, a novel microvilli-specific polytopic membrane protein of the apical A/Reference number: Z16512; PMID:98024147; PMID:9356465
A/Accession: T08881
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-858 <WEI>
A/Cross-references: EMBL:AF026269; NID:G2559003; PIDN:JAB86715.1; PID:G2559004
A/Experimental source: kidney
C/Keywords: glycoprotein; membrane protein

Query Match 9.0%; Score 86.5; DB 2; Length 858;
Best Local Similarity 22.7%; Pred. No. 6;
Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
QY 18 LHAICICQLRCSSNTPTTCORCNASVYNSVGTAILMTICGLSIIISLAIVFVFL 77
Db 117 LVGCFQCMRC-----CNK-CGGEIMQROKONAPCRKKGLSLVILVILMSIGITV 167

QY 78 RKISSEPLDEKFNKTSGLGMANIDLEKSRGD-EIIL---PRGLYEYVECTCE---- 129
Db 168 GFVANQQRTRIKGTQK-----LAKSNRDRQTLTTEPKQIDVVEGYTNTOKA 218

QY 130 ---DCIKS-----KPRVSDHCFPLPAMEGATILVTTK-TNDYCKSLPAL-- 172
Db 219 FSDLDIGISVLGRIRKIDQLKPKV-----TPVLEIRKAMATAIKOTDALONMSSLSKS 271

QY 173 ---SATEIEKISISA 183
Db 272 LODAATQLNTNLS 285

RESULT 4

hypothetical protein T24C20.80 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Nov-1999
C/Accession: T13009
R/Choisy, N.; Robert, C.; Brottier, P.; Winkler, P.; Cattolico, L.; Artiguenave, F.; Sa submitted to the Protein Sequence Database, July 1999
A/Reference number: Z17586
A/Accession: T13009
A/Molecule type: DNA
A/Residues: 1-1998 <CHO>
A/Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80
A/Experimental source: cultivar Columbia; BAC clone T24C20
C/Genetics:
A/Map position: 3
A/Insertions: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005/2;
C/Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80

Query Match 8.7%; Score 83.5; DB 2; Length 1998;
Best Local Similarity 29.4%; Pred. No. 27; Indels 43; Gaps 9;
Matches 37; Conservative 18; Mismatches 28;

QY 38 QRYCNASVYNSVKGNTAILMTCLGLSIIISLAIVFVLMFLRKISSEPLKD-EFKN--TGS 94
Db 1089 ERYCGA---NSALGTPSM---C-----SSTGPPQDSFEHFSLSGP 1122
QY 95 GLGMANIDLEKSRGDEIILPRGLEVEYVECTCEDCIKSKP-----KYSDHCFPLPAM 149
Db 1123 SLVXLSLDM--SRIGD-----RGHFFDEGSGCNGRSSAPGLNTGVNIDMCGDL--M 1173
QY 150 EEGAT 155
Db 1174 DGGAT 1179

RESULT 5

QY A57434
Db A57434
C/Species: Rattus norvegicus (Norway rat)
C/Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 04-Feb-2000
C/Accession: A57434
R/Saaki, H.; Nagura, K.; Ishino, M.; Tobioke, H.; Kotani, K.; Saaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A/Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-tyro A/Reference number: A57434; PMID:9540356; PMID:7673154
A/Accession: A57434
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1009 <SAS>
A/Cross-references: GB:D45854; NID:G1000679; PIDN:BA08290.1; PID:dl000885; PID:gl000680
C/Superfamily: ATP; phosphotransferase; tyrosine-specific protein kinases; protein kinase homolo C/Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F/423-686/Domain: protein kinase homology <KIN>
F/431-439/Region: protein kinase ATP-binding motif

Query Match 8.5%; Score 82; DB 2; Length 1009;
Best Local Similarity 26.9%; Pred. No. 18;

N/Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
 C/Species: Spodoptera frugiperda (fall armyworm)
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
 C/Accession: T43251
 R/Citeplk: M.; Klenk, H.
 Submitted to the EMBL Data Library, January 1996
 A/Description: Cloning and functional characterization of FURIN from Spodoptera frugiperda
 A/Reference number: 223368
 A/Accession: T43251
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1299 <CIB>
 A/Cross-references: EMBL:Z68888; NID:G1167859; PID:e219690; PIDN:CAA93116.1
 A/Experimental source: clone Sfurin 6; ovary
 C/Function:
 A/Description: responsible for the endoproteolytic processing of proproteins with specific
 C/Keywords: hydrolase; serine proteinase

Query Match 8.2%; Score 79.5; DB 2; Length 1299;
 Best Local Similarity 24.1%; Pred. No. 40;

Matches 39; Conservative 26; Mismatches 48; Indels 49; Gaps 11;

QY 8 CSQNEFYDSLHACICPCQLRCS-----SNTPLTCQRYCNAS-----VTNSVKGTNALI-W 57

DB 1150 CSQNEFYDSLHACICPCQLRCS-----SNTPLTCQRYCNAS-----VTNSVKGTNALI-W 1205

QY 58 TCGLGS-----LISLAV-----FVLMFLRKISSEPLKDFKNKTSGLIGMAN 101

DB 1206 GALTPLPSADAPSAVAVITIAVCAAVGLFTLVAVLQAHSPREKTRKTSVARG----- 1259

QY 102 IDLEKSRGTDEILPR-GLEYVEECTCEDCISKEKRVSDH 142

DB 1260 --VEYSR-----LPRTDVDFV-----LNSCTQDESPVEYEH 1289

RESULT 10

D64469.

potassium channel homolog - Methanococcus jannaschii

C/Species: Methanococcus jannaschii

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C/Accession: D64469

R/Bull: C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 Rosen, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996

A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese, C.
 A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A/Reference number: A64300; MUID:96337999; PMID:8688087

C/Accession: D64469

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-343 <BUL>

A/Cross-references: GB:U67575; GB:L77117; NID:G1591992; PIDN:AA99365.1; PID:G1592000; T
 C/Genetics:

A/Map position: REV1308326-1307295

C/Superfamily: conserved hypothetical protein all0993

Query Match 8.1%; Score 78.5; DB 2; Length 343;
 Best Local Similarity 20.4%; Pred. No. 13;

Matches 39; Conservative 35; Mismatches 66; Indels 51; Gaps 8;

QY 12 EYFDSLHACICPCQLRCSNTPLTCQRYCNASVTNSVKGTNALI-WTGLSLIISLAVF 71

DB 32 DFTALYFSLV-----TITTTGGDFPKFKFLRITLVVLCVGVGVVMTLPSL 80

QY 72 VLMFL-----LRKISS--EPLKDFKNTSGSLGMA-----NIDLEKSRGTD 111

DB 81 IAEPIVEGFEFEVRILKMKKIKTLKDYIICGYRLGKVGVEKFEIENIPPIADINE 140

QY 112 EIT-----LPRLETTYEECTCEDCISKEKRV-----DSDFCF-PLPMBEG 152

DB 141 DVLEKEVEKYPDKFLYIVGDAKKEVLR-KAKIDKAKGLIATLPSPADNVFLLTARELN 199

QY 153 ATIVTTKTND 163
 DB 200 PMLITAKADE 210

RESULT 11

JC5894

Killer cell inhibitory receptor p91A precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999

C/Accession: JC5894

R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya
 J. Biochem. 123, 358-368, 1998

A/Title: Genomic structures and chromosomal location of p91, a novel murine regulatory r
 A/Reference number: JC5894; MUID:98218758; PMID:9538215

A/Accession: JC5894

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-841 <YAM>

A/Cross-references: GB:AF040946

C/Comment: This protein function as inhibitory cell-surface molecule against cell activa

C/Genetics:

A/Map position: 7

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>

F/24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status p

F/636-677/Domain: transmembrane #status predicted <TM>

F/675-765/Domain: cytoplasmic #status predicted <CT>

Query Match 8.1%; Score 78; DB 2; Length 841;
 Best Local Similarity 22.7%; Pred. No. 35;

Matches 46; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

QY 9 CSQNEFYDSLHACICPCQLRCS-----SNTPLTCQRYCNASVTNSVKGTNALI-WTGLSL 64

DB 598 AONSSFYLLSSASAEVLTVSGPIETSTPPT-----MSWPLGGLMTYKALIGSV 649

QY 65 ISLAVFVLMFL--RKISSSEPLKDFKNKTSGLIGMANIDLEKSRGTDIILPRG---- 118

DB 650 AFILFPLIFILRLRRKRGKRDVQEK-----DLQSSGAEFPIRKGELQK 699

QY 119 -----LETVVECTCEDCIC-----SKPRVSDHCFPLPMBEGATIVTTKTN 162

DB 700 RNPAAQTESLVSASVDWQEDGVELNSWTPRED-----PQGET----- 741

QY 163 DYCKSLPAL--SATIEKISNR 184

DB 742 -YAQVPSRLRKAAGHVSWSMR 763

RESULT 12

D66345

hypothetical protein F16F4.10 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C/Accession: D66345

R/Ltheologis, A.; Becker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasey, T.H.; Dewar, K.;
 anzen, N.F.; Hughes, B.; Hulst, L.
 Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talion,
 Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A66141; MUID:21016719; PMID:11130712

A/Accession: D66345

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-738 <STO>

A/Cross-references: GB:AE005172; NID:G8920639; PIDN:AAE81361.1; GSPDB:GN00141

C/Genetics:

THIS PAGE BLANK (USPTO)